```
                                                  M  S  P  S  P  T  A  L  F  C  L      11
GGAGTCGACCCACGCGTCCGCAGGGCTGAGGAACC ATG TCT CCA TCC CCG ACC GCC CTC TTC TGT CTT      68

 G  L  C  L  G  R  V  P  A  Q  S  G  P  L  P  K  P  S  L  Q                        31
GGG CTG TGT CTG GGG CGT GTG CCA GCG CAG AGT GGA CCG CTC CCC AAG CCC TCC CTC CAG     128

 A  L  P  S  S  L  V  P  L  E  K  P  V  T  L  R  C  Q  G  P                        51
GCT CTG CCC AGC TCC CTG GTG CCC CTG GAG AAG CCA GTG ACC CTC CGG TGC CAG GGA CCT     188

 P  G  V  D  L  Y  R  L  E  K  L  S  S  S  R  Y  Q  D  Q  A                        71
CCG GGC GTG GAC CTG TAC CGC CTG GAG AAG CTG AGT TCC AGC AGG TAC CAG GAT CAG GCA     248

 V  L  F  I  P  A  M  K  R  S  L  A  G  R  Y  R  C  S  Y  Q                        91
GTC CTC TTC ATC CCG GCC ATG AAG AGA AGT CTG GCT GGA CGC TAC CGG TGC TCC TAC CAG     308

 N  G  S  L  W  S  L  P  S  D  Q  L  E  L  V  A  T  G  V  F                       111
AAC GGA AGC CTC TGG TCC CTG CCC AGC GAC CAG CTG GAG CTC GTT GCC ACG GGA GTT TTT     368

 A  K  P  S  L  S  A  Q  P  G  P  A  V  S  S  G  G  D  V  T                       131
GCC AAA CCC TCG CTC TCA GCC CAG CCC GGC CCG GCG GTG TCG TCA GGA GGG GAC GTA ACC     428

 L  Q  C  Q  T  R  Y  G  F  D  Q  F  A  L  Y  K  E  G  D  P                       151
CTA CAG TGT CAG ACT CGG TAT GGC TTT GAC CAA TTT GCT CTG TAC AAG GAA GGG GAC CCT     488

 A  P  Y  K  N  P  E  R  W  Y  R  A  S  F  P  I  I  T  V  T                       171
GCG CCC TAC AAG AAT CCC GAG AGA TGG TAC CGG GCT AGT TTC CCC ATC ATC ACG GTG ACC     548

 A  A  H  S  G  T  Y  R  C  Y  S  F  S  S  R  D  P  Y  L  W                       191
GCC GCC CAC AGC GGA ACC TAC CGA TGC TAC AGC TTC TCC AGC AGG GAC CCA TAC CTG TGG     608

 S  A  P  S  D  P  L  E  L  V  V  T  G  T  S  V  T  P  S  R                       211
TCG GCC CCC AGC GAC CCC CTG GAG CTT GTG GTC ACA GGA ACC TCT GTG ACC CCC AGC CGG     668

 L  P  T  E  P  P  S  S  V  A  E  F  S  E  A  T  A  E  L  T                       231
TTA CCA ACA GAA CCA CCT TCC TCG GTA GCA GAA TTC TCA GAA GCC ACC GCT GAA CTG ACC     728

 V  S  F  T  N  K  V  F  T  T  E  T  S  R  S  I  T  T  S  P                       251
GTC TCA TTC ACA AAC AAA GTC TTC ACA ACT GAG ACT TCT AGG AGT ATC ACC ACC AGT CCA     788

 K  E  S  D  S  P  A  G  P  A  R  Q  Y  Y  T  K  G  N  L  V                       271
AAG GAG TCA GAC TCT CCA GCT GGT CCT GCC CGC CAG TAC TAC ACC AAG GGC AAC CTG GTC     848

 R  I  C  L  G  A  V  I  L  I  I  L  A  G  F  L  A  E  D  W                       291
CGG ATA TGC CTC GGG GCT GTG ATC CTA ATA ATC CTG GCG GGG TTT CTG GCA GAG GAC TGG     908

 H  S  R  R  K  R  L  R  H  R  G  R  A  V  Q  R  P  L  P  P                       311
CAC AGC CGG AGG AAG CGC CTG CGG CAC AGG GGC AGG GCT GTG CAG AGG CCG CTT CCG CCC     968

 L  P  P  L  P  Q  T  R  K  S  H  G  G  Q  D  G  G  R  Q  D                       331
CTG CCG CCC CTC CCG CAG ACC CGG AAA TCA CAC GGG GGT CAG GAT GGA GGC CGA CAG GAT    1028

 V  H  S  R  G  L  C  S  *                                                         340
GTT CAC AGC CGC GGG TTA TGT TCA TGA                                               1055
```

FIGURE 1a

CCGCTGAACCCCAGGCACGGTCGTATCCAAGGGAGGGATCATGGCATGGGAGGCGACTCAAAGACTGGCGTGTGTGGAG 1134

CGTGGAAGCAGGAGGGCAGAGGCTACAGCTGTGGAAACGAGGCCATGCTGCCTCCTCCTGGTGTTCCATCAGGGAGCCG 1213

TTCGGCCAGTGTCTGTCTGTCTGTCTGCCTCTCTGTCTGAGGGCACCCTCCATTTGGGATGGAAGGAATCTGTGGAGAC 1292

CCCATCCTCCTCCCTGCACACTGTGGATGACATGGTACCCTGGCTGGACCACATACTGGCCTCTTTCTTCAACCTCTCT 1371

AATATGGGCTCCAGACGGATCTCTAAGGTTCCCAGCTCTCAGGGTTGACTCTGTTCCATCCTCTGTGCAAAATCCTCCT 1450

GTGCTTCCCTTTGGCCCTCTGTGCTCTTGTCTGGTTTTCCCCAGAAACTCTCACCCTCACTCCATCTCCCACTGCGGTC 1529

TAACAAATCTCCTTTCGTCTCTCAGAACGGGTCTTGCAGGCAGTTTGGGTATGTCATTCATTTTCCTTAGTGTAAAACT 1608

AGCACGTTGCCCCGCTTCCCTTCACATTAGAAAACAAGATCAGCCTGTGCAACATGGTGAAACCTCATCTCTACCAACAA 1687

AACAAAAAAACACAAAAATTAGCCAGGTGTGGTGGTGCATCCCTATACTCCCAGCAACTCGGGGGGCTGAGGTGGGAGA 1766

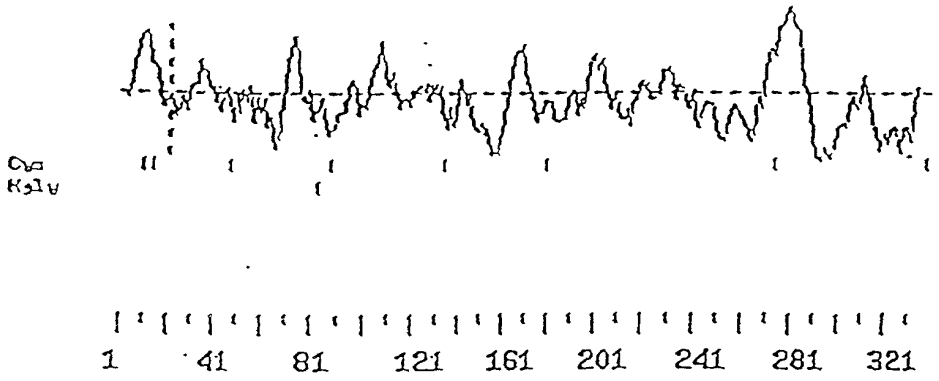
ATGGCTTGAGCCTGGGAGGCAGAGGTTGCAGTGAGCTGAGATCACACCACTGCACTCTAGCTCGGGTGACGAAGCCTGA 1845

CCTTGTCTCAAAAAATACAGGGATGAATATGTCAATTACCCTGATTTGATCATAGCACGTTGTATACATGTACTGCAAT 1924

ATTGCTGTCCACCCCATAAATATGTACAATTATGTATACATTTTTAAAATCATAAAAATAAGATAATGAAAAAAAAAAA 2003

AAAAAAAAAAAAAAAGGGCGGGCCGCTAGACTAGTCTAGAGAACA 2047

FIGURE 1b



MSPSPTALFCLGLCLGRVPAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLE
KLSSSRYQDQAVLFIPAMKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQP
GPAVSSGGDVTLQCQTRYGFDQFALYKEGDPAPYKNPERWYRASFPIITVTAAHSGTYRC
YSFSSRDPYLWSAPSDPLELVVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFT
TETSRSITTSPKESDSPAGPARQYYTKGNLVRICLGAVILIILAGFLAEDWHSRRKRLRH
RGRAVQRPLPPLPPLPQTRKSHGGQDGGRQDVHSRGLCS

FIGURE 2

```
ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> U91928 ORF                                          1893 aa vs.
> hT268 ORF                                           1017 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
37.7% identity;          Global alignment score: -8

               10         20         30         40         50         60         70
inputs ATGACGCCCGCCCTCACAGCCCTGCTCTGCCTTGGGCTGAGTCTGGGCCCCAGGACCCGCGTGCAGGCAG
       :::.: ::  :::  :: :::::  :::: ::::::::::.::::::: :: .: .:: ::  :::::. .:
       ATGTCTCCATCCCCGACCGCCCTCTTCTGTCTTGGGCTGTGTCTGGGGCG-TGTGCCAGC--GCAGAGTG
               10         20         30         40         50           60

               80         90        100        110        120        130
inputs GGCCCTTCCCCAAACCCACCCTCTGGGCTGAGCCAGGCTCTGTGAT-CAGCTGGGGGAGCCCCGTGACCA
       :.::  ::::::::.:::.::::: .:::: .::: .:::::  ::.: :  :::::.:.::::  ::::::
       GACCGCTCCCCAAGCCCTCCCTCCAGGCTCTGCCCAGCTCCCTGGTGCCCCTGGAGAAGCCA-GTGACCC
        70         80         90        100        110        120        130

     140        150        160        170        180        190        200
inputs TCTGGTGTCAGGGGAGCCTGGAGGCCCAGGAGTACCGACTGGATAAAGAGGGAAGCCCAGAGCCCTTGGA
       :: :::: :::::  .:::      ::.:: ::.  ::: :..          ::: .:::     ...
       TCCGGTGCCAGGG--ACCT------CCGGGCGTG--GACCTGTA--------CCGCCTGGAG-----AAG
        140          150              160        170              180

     210        220        230        240        250        260        270
inputs CAGAAATAACCCACTGGAACCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGCACCATGCG
       :.::..:  :: .:.::.::: :.::.:: ::: .   ::: :::::::. :::::: .... . :. ::
       CTGAGTT--CCAGCAGGTACC-AGGATCA-GGCAGTCCTCTTCATCCCGGCCATGAAGAGAAGTCTGGCT
           190          200        210        220        230        240

     280        290        300        310          320        330        340
inputs GGGAGATACCGCTGCCACTATTACAGCTCTGCAG--GCTGGTCAGAGCCCAGCGACCCCCTGGAGCTGGT
       ::. : :::::::::  :::   ::: .: : ::   ::::::  .:::::::::::  :::::::: ::
       GGACGCTACCGCTGCTCCTAC--CAGAACGGAAGCCTCTGGTCCCTGCCCAGCGACCAGCTGGAGCTCGT
     250        260        270        280        290        300        310

       350        360        370        380        390        400        410
inputs GATGACAGGATTCTACAACAAACCCACCCTCTCAGCCCTGCCCAGCCCTGTGGTGGCCTCAGGGGGGAAT
        . ::.::: : :. . :::::::.: ::::::::::.::::.:::: : :::: : :::::.:::.:
       TGCCACGGGAGTTTTTGCCAAACCCTCGCTCTCAGCCCAGCCCCGGCCCCGGCGGTGTCGTCAGGAGGGGAC
       320        330        340        350        360        370        380

       420        430        440        450        460        470        480
inputs ATGACCCTCCGATGTGGCTCACAGAAGGGATATCACCATTTTGTTCTGATGAAGGAAGGAGAACACCAGC
       .:.:::::: :..::: . .:.:.:.: :: :.: ::::.:::: :::::.. ::::::::
       GTAACCCTACAGTGTCAGACTCGGTATGGCTTTGACCAATTTGCTCTGTACAAGGAAGG----------
       390        400        410        420        430        440

       490        500        510        520        530        540        550
inputs TCCCCCCGACCCTGGACTCACAGCAGCTCCACAGTGGGGGGTTCCAGGCCCTGTTCCCTGTGGGCCCCGT
       ::::::::                                :  :::::.                  :..
```

FIGURE 3a

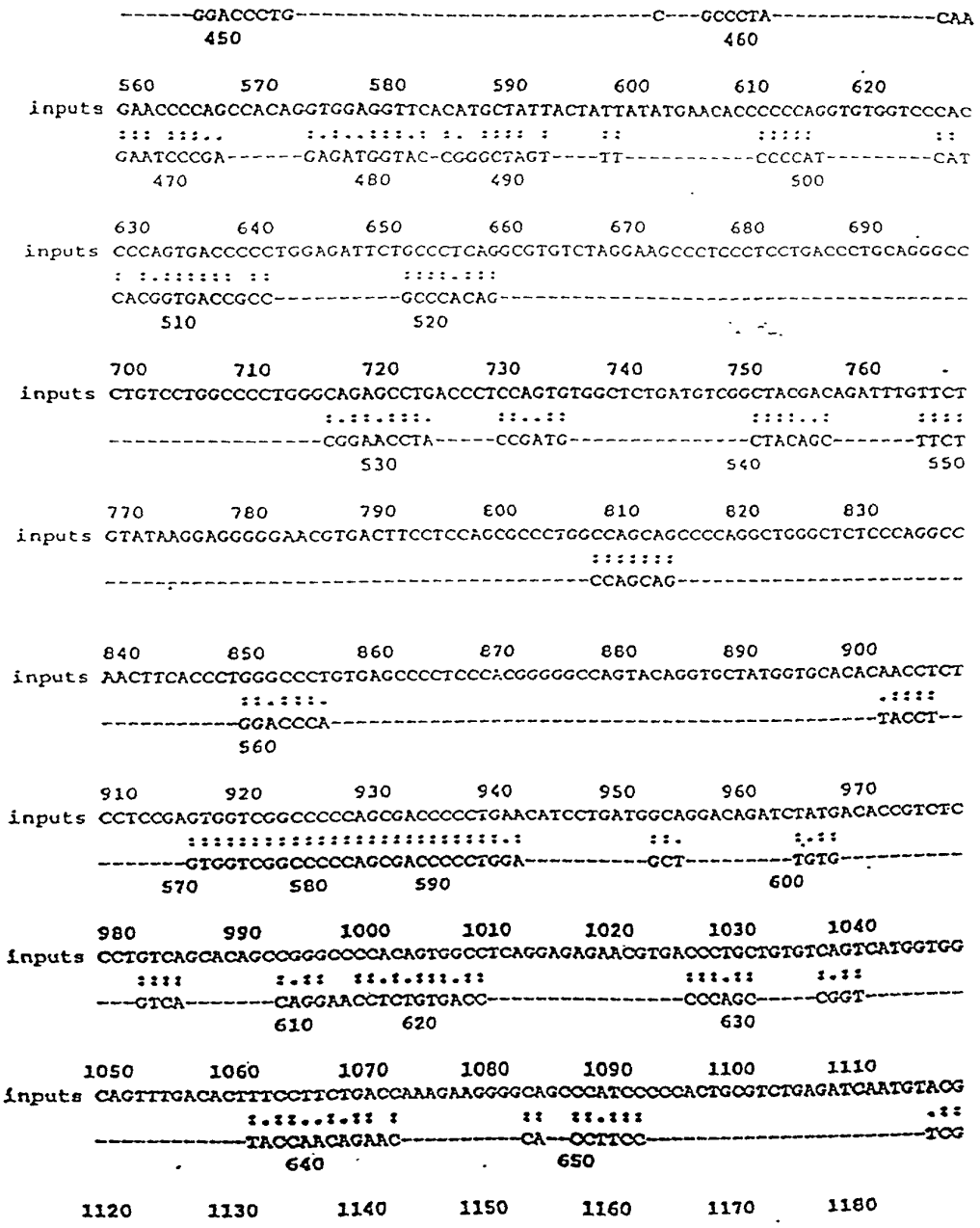


FIGURE 3b

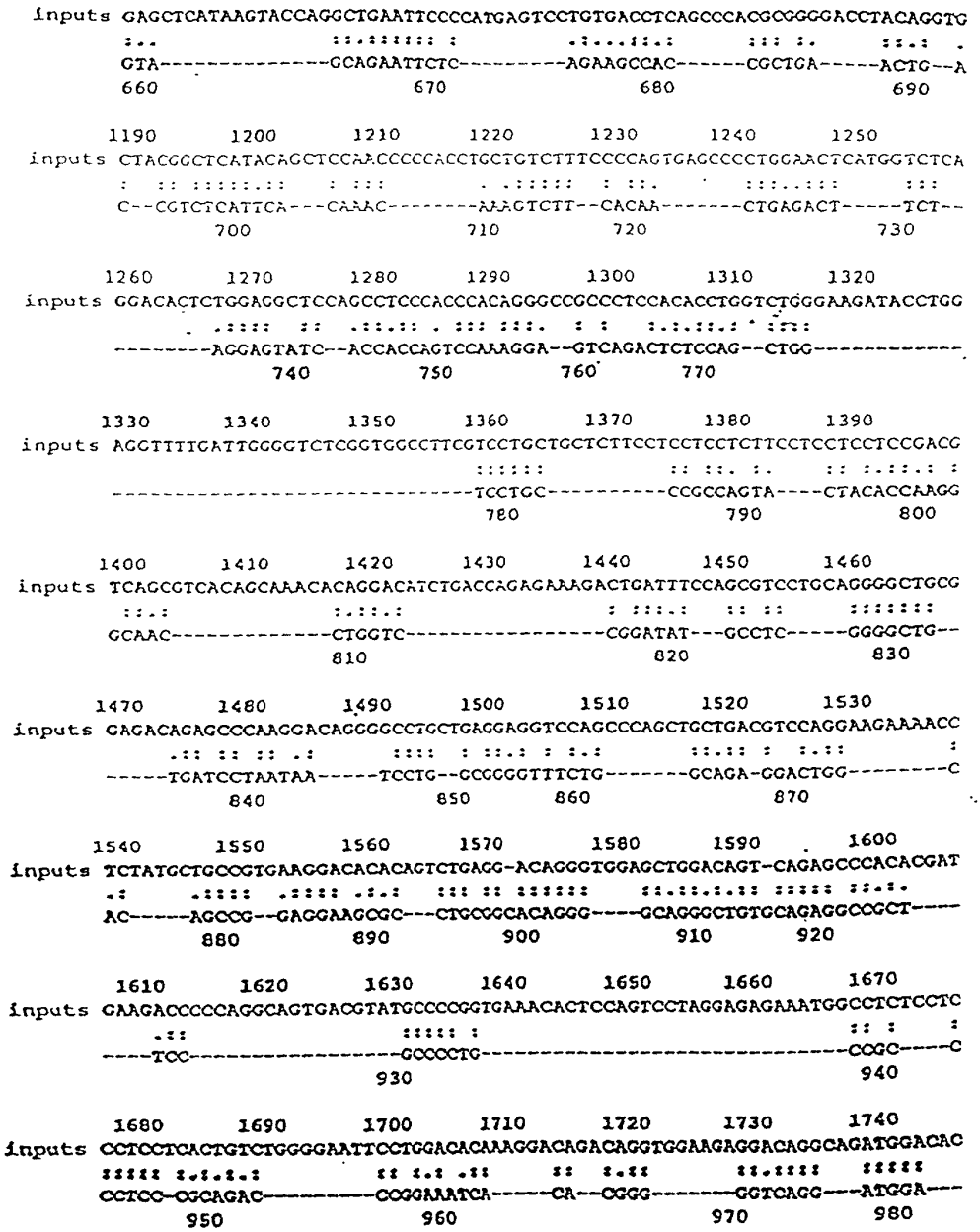


FIGURE 3c

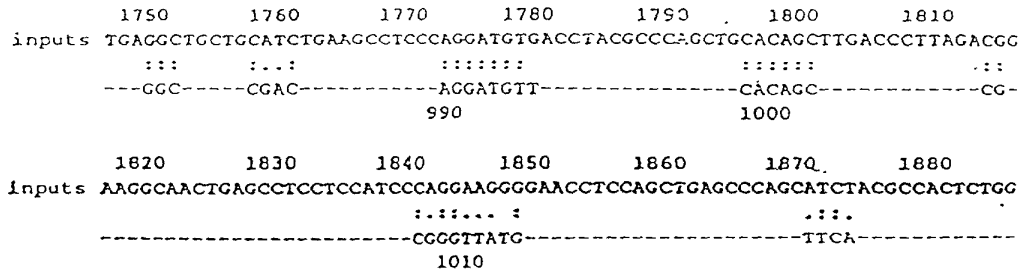

1750 1760 1770 1780 1790 1800 1810
inputs TGAGGCTGCTGCATCTGAAGCCTCCCAGGATGTGACCTACGCCCAGCTGCACAGCTTGACCCTTAGACGG
---GGC-----CGAC----------AGGATGTT----------CACAGC----------CG-
990 1000
1820 1830 1840 1850 1860 1870 1880
inputs AAGGCAACTGAGCCTCCTCCATCCCAGGAAGGGGAACCTCCAGCTGAGCCCAGCATCTACGCCACTCTGG
----------CGGGTTATG----------TTCA----------
1010
1890
inputs CCATCCAC

FIGURE 3d

```
ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> hT268 a.a.                                        339 aa vs.
> GenPept U91928 - Human clone HL9 monocyte inhib   631 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
23.0% identity;          Global alignment score: -642

               10         20         30         40         50         60
inputs MSPSPTALFCLGLCLG-RVPAQSGPLPRPSLQALPSSLVPLERPVTLRCQGPPGVDLYRLEKLSSS----
       :.:. :::.:::: :: :. .:.::.:::.: : :.:...   :::.:::. .. :::.: .:.
       MTPALTALLCLGLSLGPRTRVQAGPFPKPTLWAEPGSVISWGSPVTIWCQGSLEAQEYRLDKEGSPEPLD
               10         20         30         40         50         60         70

               70         80         90        100        110        120        130
inputs RYQ-----DQAVLFIPARKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDV
       : .     ..: . ::.:    :::::: : ... :: :::.:::: :: ..::.::: :.:.:.:::..
       RHNPLEPKNKARFSIPSMTEHHAGRYRCHYYSSAGWSEPSDPLELVMTGFYNKPTLSALPSPVVASGGNM
               80         90        100        110        120        130        140

inputs TLQCQT-------------------------------------------------RY----------------
       ::.: .                                                 :.
       TLRCGSQKGYHHFVLMKEGEHQLPRTLDSQQLHSGGFQALFPVGPVNPSHRWRFTCYYYYHNTPQVWSHP
              150        160        170        180        190        200        210

                                                 140        150
inputs ------------------------------------------GFDQFALYKEGDP------------------
                                                 :.:.:.:::::.
       SDPLEILPSGVSRKPSLLTLQGPVLAPGQSLTLQCGSDVGYDRFVLYKEGERDFLQRPGQQPQAGLSQAN
              220        230        240        250        260        270        280

                                                                              160
inputs -----------APYK---------------HP-----------------------------------ERW--
                 ..:.               .:                                     . :
       FTLGPVSPSHGGQYRCYGAHNLSSEWSAPSDPLNILMAGQIYDTVSLSAQPGPTVASGENVTLLCQSWWQ
              290        300        310        320        330        340        350

                                          170        180        190        200
inputs ---------------------------YRASFPIITVTAAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTG
                                   :.: ::.  ::.::.::::::.  : .: : : ::.::::.:.:
       FDTFLLTKEGAAHPPLRLRSHYGAHKYQAEFPHSPVTSAHAGTYRCYGSYSSNPHLLSFPSEPLELMVSG
              360        370        380        390        400        410        420

     210        220        230                   240        250        260
inputs TSVTPSRLPTEPPSS--VAEFSEATAELTVSFTNKVF---------TTETSRSITTSPKESD--SPAGPA-
       : .: :: :::.  .. . :.  ..:.:.  .:           :.  :.... .:   :::.:
       HSGGSSLPPTGPPSTPGLGRYLEVLIGVSVAFVLLLFLLLFLLLRRQRHSKHRTSDQRKTDFQRPAGAAE
              430        440        450        460        470        480        490

            270        280        290
inputs RQYYTKGNLVRICLGAVIL-----IILAGFLAEDW----------------------HSRRKR--------
       .  .: : :  .: .       . .  .::.                        ::  .:
```

FIGURE 4a

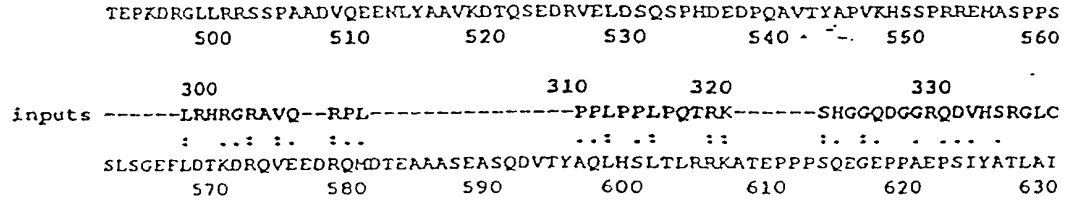

TEPKDRGLLRRSSPAADVQEENLYAAVKDTQSEDRVELDSQSPHDEDPQAVTYAPVKHSSPRREMASPPS
500 510 520 530 540 550 560
300 310 320 330
inputs ------LRHRGRAVQ--RPL----------PPLPPLPQTRK------SHGGQDGGRQDVHSRGLC
SLSGEFLDTKDRQVEEDRQMDTEAAASEASQDVTYAQLHSLTLRRKATEPPPSQEGEPPAEPSIYATLAI
570 580 590 600 610 620 630
inputs S
H

FIGURE 4b

```
Alignments of top-scoring domains:
ig: domain 1 of 2, from 41 to 90: score 4.1, E = 6.1
                 *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                    . + vtL+C+          + v  y +  k  ++        .r++ +
bT268     41    ERPVTLRCQQGP------PGVDLY-RLEKlSSS--------RYQDQ-- 70

                anlsegrfsissltLtissvekeDsGtYtCvv<-*
                          ++L i   +++ +G Y+C
bT268     71 ------------AVLFIPAMKRSLAGRYRCSY    90
```

FIGURE 5A

```
ig: domain 2 of 2, from 127 to 182: score 19.1, E = 0.1
                   *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                      G++vtL+C+++    +  ++  y k+g++ +     y+++
        hT268   127   GGDVTLQCQTR---YGFDQFALY-KEGDpAP-----YKNPERWYR-- 162

                   anlsegrfsissltLtissvekeDsGtYtCvv<-*
                              ++++i++v++  sGtY+C
        hT268   163 ------------ASFPIITVTAAHSGTYRCYS    182
```

FIGURE 5B

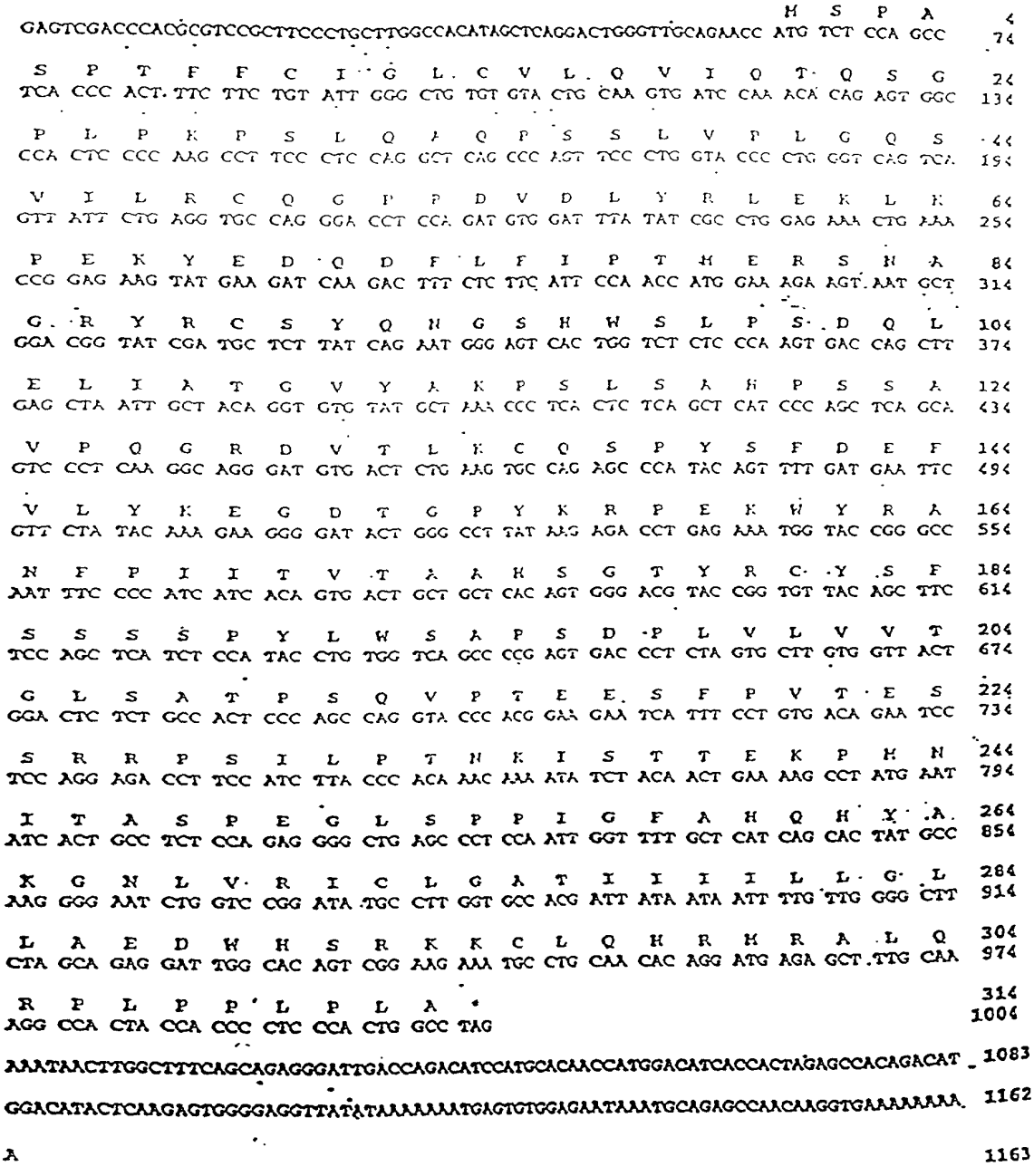

H S P A
GAGTCGACCCACGCGTCCGCTTCCCTGCTTGGCCACATAGCTCAGGACTGGGTTGCAGAACC ATG TCT CCA GCC
S P T F F C I G L C V L Q V I Q T Q S G
TCA CCC ACT TTC TTC TGT ATT GGG CTG TGT GTA CTG CAA GTG ATC CAA ACA CAG AGT GGC
P L P K P S L Q A Q P S S L V P L G Q S
CCA CTC CCC AAG CCT TCC CTC CAG GCT CAG CCC AGT TCC CTG GTA CCC CTG GGT CAG TCA
V I L R C Q G P P D V D L Y R L E K L K
GTT ATT CTG AGG TGC CAG GGA CCT CCA GAT GTG GAT TTA TAT CGC CTG GAG AAA CTG AAA
P E K Y E D Q D F L F I P T H E R S N A
CCG GAG AAG TAT GAA GAT CAA GAC TTT CTC TTC ATT CCA ACC ATG GAA AGA AGT AAT GCT
G R Y R C S Y Q N G S H W S L P S D Q L
GGA CGG TAT CGA TGC TCT TAT CAG AAT GGG AGT CAC TGG TCT CTC CCA AGT GAC CAG CTT
E L I A T G V Y A K P S L S A H P S S A
GAG CTA ATT GCT ACA GGT GTG TAT GCT AAA CCC TCA CTC TCA GCT CAT CCC AGC TCA GCA
V P Q G R D V T L K C Q S P Y S F D E F
GTC CCT CAA GGC AGG GAT GTG ACT CTG AAG TGC CAG AGC CCA TAC AGT TTT GAT GAA TTC
V L Y K E G D T G P Y K R P E K W Y R A
GTT CTA TAC AAA GAA GGG GAT ACT GGG CCT TAT AAG AGA CCT GAG AAA TGG TAC CGG GCC
N F P I I T V T A A H S G T Y R C Y S F
AAT TTC CCC ATC ATC ACA GTG ACT GCT GCT CAC AGT GGG ACG TAC CGG TGT TAC AGC TTC
S S S S P Y L W S A P S D P L V L V V T
TCC AGC TCA TCT CCA TAC CTG TGG TCA GCC CCG AGT GAC CCT CTA GTG CTT GTG GTT ACT
G L S A T P S Q V P T E E S F P V T E S
GGA CTC TCT GCC ACT CCC AGC CAG GTA CCC ACG GAA GAA TCA TTT CCT GTG ACA GAA TCC
S R R P S I L P T N K I S T T E K P K N
TCC AGG AGA CCT TCC ATC TTA CCC ACA AAC AAA ATA TCT ACA ACT GAA AAG CCT ATG AAT
I T A S P E G L S P P I G F A H Q H Y A
ATC ACT GCC TCT CCA GAG GGG CTG AGC CCT CCA ATT GGT TTT GCT CAT CAG CAC TAT GCC
K G N L V R I C L G A T I I I I L L G L
AAG GGG AAT CTG GTC CGG ATA TGC CTT GGT GCC ACG ATT ATA ATA ATT TTG TTG GGG CTT
L A E D W H S R K K C L Q H R K R A L Q
CTA GCA GAG GAT TGG CAC AGT CGG AAG AAA TGC CTG CAA CAC AGG ATG AGA GCT TTG CAA
R P L P P L P L A
AGG CCA CTA CCA CCC CTC CCA CTG GCC TAG
AAATAACTTGGCTTTCAGCAGAGGGATTGACCAGACATCCATGCACAACCATGGACATCACCACTAGAGCCACAGACAT
GGACATACTCAAGAGTGGGGAGGTTATATAAAAAAAATGAGTGTGGAGAATAAATGCAGAGCCAACAAGGTGAAAAAAAAA
A

FIGURE 6

MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRL
EKLKPEKYEDQDFLFIPTMERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAH
PSSAVPQGRDVTLKCQSPYSFDEFVLYKEGDTGPYKRPEKWYRANFPIITVTAAHSGTYR
CYSFSSSSPYLWSAPSDPLVLVVTGLSATPSQVPTEESFPVTESSRRPSILPTNKISTTE
KPMNITASPEGLSPPIGFAHQHYAKGNLVRICLGATIIIILLGLLAEDWHSRKKCLQHRM
RALQRPLPPLPLA

09809809 - 010599

FIGURE 7

```
ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> U91928 ORF                                          1893 aa vs.
> mT268 ORF                                            939 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
34.3% identity;          Global alignment score: -836

                10        20        30        40        50        60        70
inputs ATGACGCCCGCCCTCACAGCCCTGCTCTGCCTTGGGCTGAGTCTGGGCCCCAGGACCCGCGTGCAGGCAG
       ::::: :: ::: :::: ::    .::  :::   ::::.:
       ATGTCTCCAGCC-TCAC--CC----ACTTTCTT---CTGTAT----------------------------
                10                20        30

                80        90       100       110       120       130       140
inputs GGCCCTTCCCCAAACCCACCCTCTGGGCTGAGCCAGGCTCTGTGATCAGCTGGGGGAGCCCCGTGACCAT
                                 :::::::           :::::..:.::
       ------------------------TGGGCTG----------TGTGTACTGC--------------------
                                          40

                150       160       170       180       190       200       210
inputs CTGGTGTCAGGGGAGCCTGGAGGCCCAGGAGTACCGACTGGATAAAGAGGGAAGCCCAGAGCCCTTGGAC
                                  :.:.:..::                 ::.: :::::    :::
       --------------------------AAGTGATCC----------------AAACACAGAG----TGG--
                                 50                        60            70

                220       230       240       250       260       270       280
inputs AGAAATAACCCACTGGAACCCAAGAACAAGGCCAGATTCTCCATCCCATCCATGACAGAGCACCATGCGG
                :::::::    :::     ::::          ::.:::: :::: :
       --------CCCACT----CCC-----CAAG----------CCTTCCC-TCCAGG-----------------
                          80                        90

                290       300       310       320       330       340       350
inputs GGAGATACCGCTGCCACTATTACAGCTCTGCAGGCTGGTCAGAGCCCAGCGACCCCCTGGAGCTGGTGAT
                : :.:::                          :::. :::.: :. :::::::. :.:
       --------CTCAGCC-----------------------CAGTTCCCTG-GTACCCCTGGGTCAG------
                100                              110       120

                360       370       380       390       400       410       420
inputs GACAGGATTCTACAACAAACCCACCCTCTCAGCCCTGCCCAGCCCTGTGGTGGCCTCAGGGGGGAATATG
                .:::  :: :.:                             ::.:::: :  ::::::.
       -TCAG--TTATTC-----------------------------------TGAGGTG-C--CAGGGA---------
      130                                       140       150

                430       440       450       460       470       480
inputs ACCCTCC-GATGTGGCTCACAGAAGGGATATCACCATTTTGTTCTGATGAAGGAAGGAGAACACCAGCTC
         ::::: :::::::          :  :::::.::.  . ...:::::..
       --CCTCCAGATGTGG---------ATTTATATCGCCTGGAGAAACTGAAA----------------------
            160               170       180       190

     490       500       510       520       530       540       550
inputs CCCCGGACCCTGGACTCACAGCAGCTCCACAGTGGGGGGTTCCAGGCCCTGTTCCCTGTGGGCCCCGTGA
        :::::     ::              :::. :..:.:: ::.:    ::: ::          :.:
```

FIGURE 8a

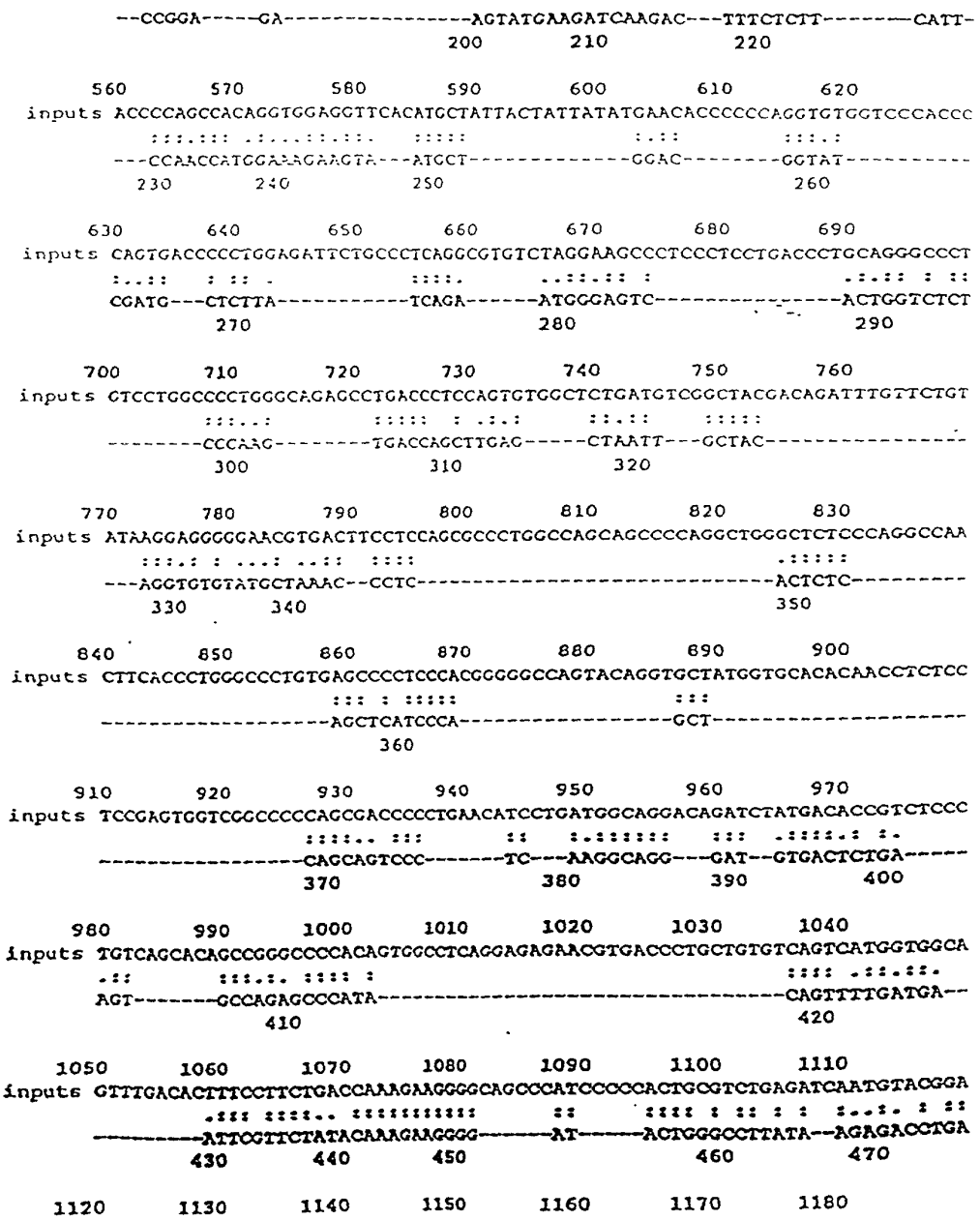


FIGURE 8b

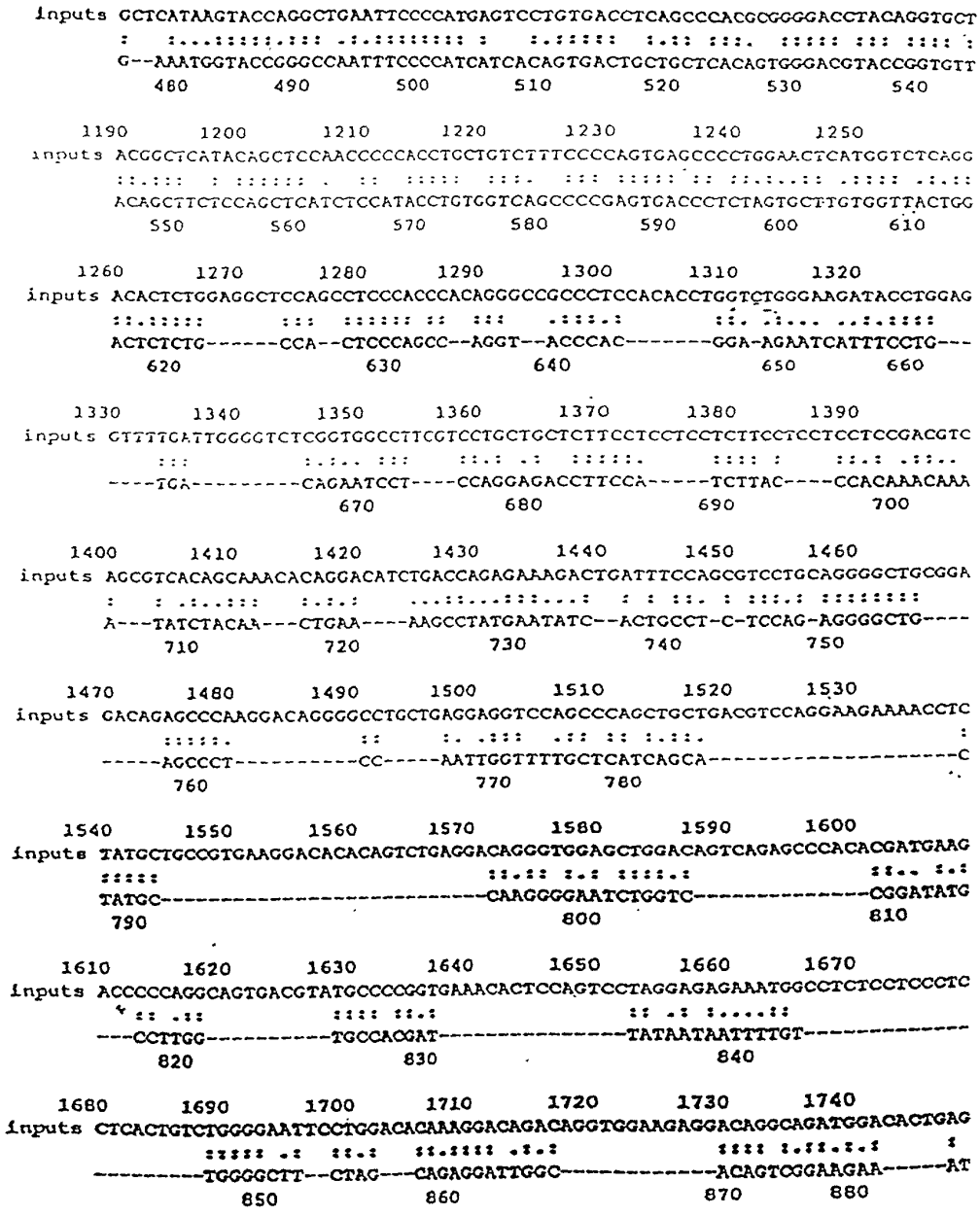


FIGURE 8c

```
     1750       1760       1770       1780       1790       1800       1810
inputs GCTGCTGCATCTGAAGCCTCCCAGGATGTGACCTACGCCCAGCTGCACAGCTTGACCCTTAGACGGAAGG
       ::  ::::::.:.          ::::::::.::                   :::: .:         .::::
       GC--CTGCAACA----------CAGGATGAGA------------------GCTTTGC---------AAAGG
             890                 900                        910

     1820       1830       1840       1850       1860       1870       1880
inputs CAACTGAGCCTCCTCCATCCCAGGAAGGGGAACCTCCAGCTGAGCCCAGCATCTACGCCACTCTGGCCAT
       : :::.     ::.::                 :::::                          :.:::::::
       CCACTA-----CCACC----------------CCTCC----------------------CACTGGCC--
         920                            930

    1890
inputs CCAC

       ----
```

FIGURE 8d

```
ALIGN calculates a global alignment of two sequences
 version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> mT268 a.a.                                          313 aa vs.
> GenPept U91928 - Human clone HL9 monocyte inhib     631 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
20.3% identity;          Global alignment score: -802

                10        20        30        40        50        60
inputs MSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRLEKL-KPERNA
       :.::  ...:.:: . . ...:.::.:::.: :.:.:... : .:...:::. ... ::::.:   ::  .
       MTPALTALLCLGLSLGPRTRVQAGPFPKPTLWAEPGSVISWGSPVTIWCQGSLEAQEYRLDKEGSPEPLD
                10        20        30        40        50        60        70

      70                80        90       100       110       120       130
inputs DQDFL--------F-IPTMERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAHPSSAVPQGRDV
        .. :       : ::.:   .:::::: : ... :: :::.:::. :: :.::.::: ::..:. : ..
       RNNPLEPKNKARFSIPSMTEHHAGRYRCHYYSSAGHSEPSDPLELVMTGFYNKPTLSALPSPVVASGGNM
                80        90       100       110       120       130       140

inputs TLKC--QSPY-----------------------------------------------------------
       ::.:  :  :
       TLRCGSQKGYHMFVLMKEGEHQLPRTLDSQQLHSGGFQALFPVGPVMPSHRWRFTCYYYYMNTPQVWSHP
              150       160       170       180       190       200       210

                                                140       150
inputs ------------------------------------------SFDEFVLYKEGD-----------------
                                                  ..: :::::::.
       SDPLEILPSGVSRKPSLLTLQGPVLAPGQSLTLQCGSDVGYDRFVLYKEGERDFLQRPGQQPQAGLSQAN
              220       230       240       250       260       270       280

                                                                          160
inputs ----------TGPYK-----------------------------------RP--------------EKW--
                 :.:.                                      .:              . :
       FTLGPVSPSHGGQYRCYGAHNLSSEWSAPSDPLNILMAGQIYDTVSLSAQPGPTVASGENVTLLCQSHMQ
              290       300       310       320       330       340       350

                                        170       180       190       200
inputs --------------------------YRANFPIITVTAAHSGTYRCYSFSSSSPYLWSAPSDPLVLVVTG
                                 :.:.::.  ::.::.::::::.  ::.: : : ::.:: :.:.:
       FDTFLLTKEGAAHPPLRLRSHYGAHKYQAEFPHSPVTSAHAGTYRCYGSYSSNPHLLSFPSEPLELMVSG
              360       370       380       390       400       410       420

         210                       220
inputs LSATPSQVPTEES-----------------FPV-------------------------------------
       :. .: ::  .                   : .
       HSGGSSLPPTGPPSTPGLGRYLEVLIGVSVAFVLLLFLLLFLLLRRQRHSKHRTSDQRKTDFQRPAGAAE
              430       440       450       460       470       480       490

                .          230       240       250       260       270
inputs TESS-----RRPS----------ILPTNKISTTEKPHNI-TASPEGLSP-PIGFAH--QHYAKGNLVR--I
       ::.      ::.:          . .. : . .:  ... . :: . .: .. .:   .  .. ...
```

FIGURE 9a

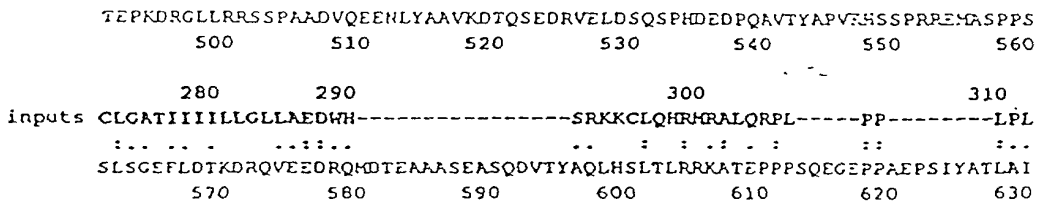

TEPKDRGLLRRSSPAADVQEENLYAAVKDTQSEDRVELDSQSPHDEDPQAVTYAPVRHSSPRREMASPPS
500 510 520 530 540 550 560
280 290 300 310
inputs CLGATIIIILLGLLAEDWH----------SRKKCLQHRMRALQRPL-----PP--------LPL
SLSGEFLDTKDRQVEEDRQMDTEAAASEASQDVTYAQLHSLTLRRKATEPPPSQEGEPPAEPSIYATLAI
570 580 590 600 610 620 630
inputs ?.
H

FIGURE 9b

```
Alignments of top-scoring domains:
ig: domain 1 of 2, from 42 to 91: score 10.2, E = 1.4
                   *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
          mT268    42    G+sv L+C+      ++v  y +  k ++          +++e +
                         GQSVILRCQGP------PDVDLY-RLERLKP--------EKYEDQ-- 71

                   anlsegrfsissltLtissvekeDsGtYtCvv<-*
          mT268    72 ------------DFLFIPTMERSNAGRYRCSY    91
```

FIGURE 10A

```
ig: domain 2 of 2, from 128 to 183: score 9.6, E = 1.6
                   *->GesvtLtCsvsgfgppgvsvtWyfkngk.lgpsllgysysrlesgek
                      G +vtL C++          ++  y k+g++ +        y+r+e   +
        mT268   128   GRDVTLKCQSP---YSFDEFVLY-KEGDtGP-------YKRPEKW-Y 162

                   anlsegrfsissltLtissvekeDsGtYtCvv<-*
                   +   .           ++i++v++  sGtY+C
        mT268   163 RA----------NFPIITVTAAHSGTYRCYS     183
```

FIGURE 10B

ALIGN calculates a global alignment of two sequences
version 2.0uPlease cite: Myers and Miller, CABIOS (1989)
> hT268 a.a. 339 aa vs.
> mT268 a.a. 313 aa
scoring matrix: pam120.mat, gap penalties: -12/-4
64.4% identity; Global alignment score: 1011
inputs HSPSPTALFCLGLCLGRV-PAQSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVDLYRLEKLSSSRYQD
HSPASPTFFCIGLCVLQVIQTQSGPLPKPSLQAQPSSLVPLGQSVILRCQGPPDVDLYRLEKLKPEKYED
inputs QAVLFIPAKKRSLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYG
QDFLFIPTHERSNAGRYRCSYQNGSHWSLPSDQLELIATGVYAKPSLSAHPSSAVPQGRDVTLKCQSPYS
inputs FDQFALYKEGDPAPYKNPERWYRASFPIITVTAAHSGTYRCYSFSSRDPYLWSAPSDPLELVVTGTSVTP
FDEFVLYKEGDTGPYKRPEKWYRANFPIITVTAAHSGTYRCYSFSSSSPYLWSAPSDPLVLVVTGLSATP
inputs SRLPTEPPSSVAEFSEATAELTVSFTNKVFTTETSRSITTSPKESDSPAGPARQYYTKGNLVRICLGAVI
SQVPTEESFPVTESSRRPSILP---TNKISTTEKPMNITASPEGLSPPIGFAHQHYAKGNLVRICLGATI
inputs LIILAGFLAEDWHSRRKRLRHRGRAVQRPLPPLPPLPQTRKSHGGQDGGRQDVHSRGLCS
IIILLGLLAEDWHSRKKCLQHRHRALQRPLPPLP-LA----------
10 20 30 40 50 60
70 80 90 100 110 120 130
140 150 160 170 180 190 200
210 220 230 240 250 260 270
280 290 300 310 320 330

FIGURE 11

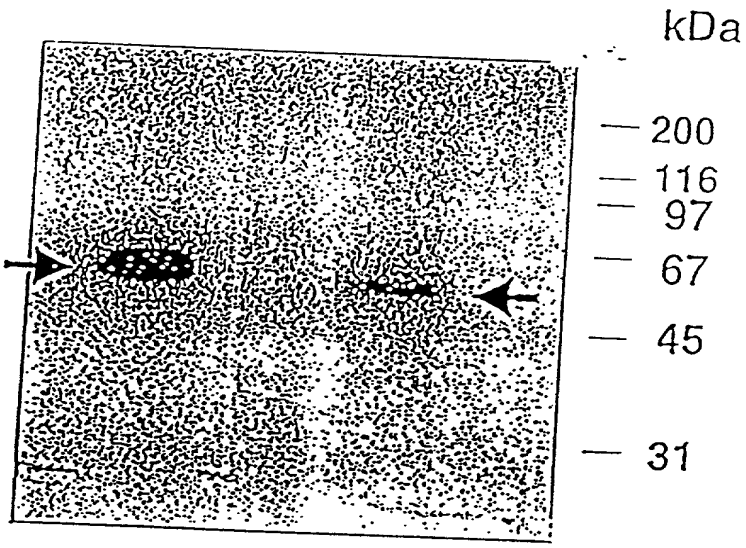


FIGURE 12

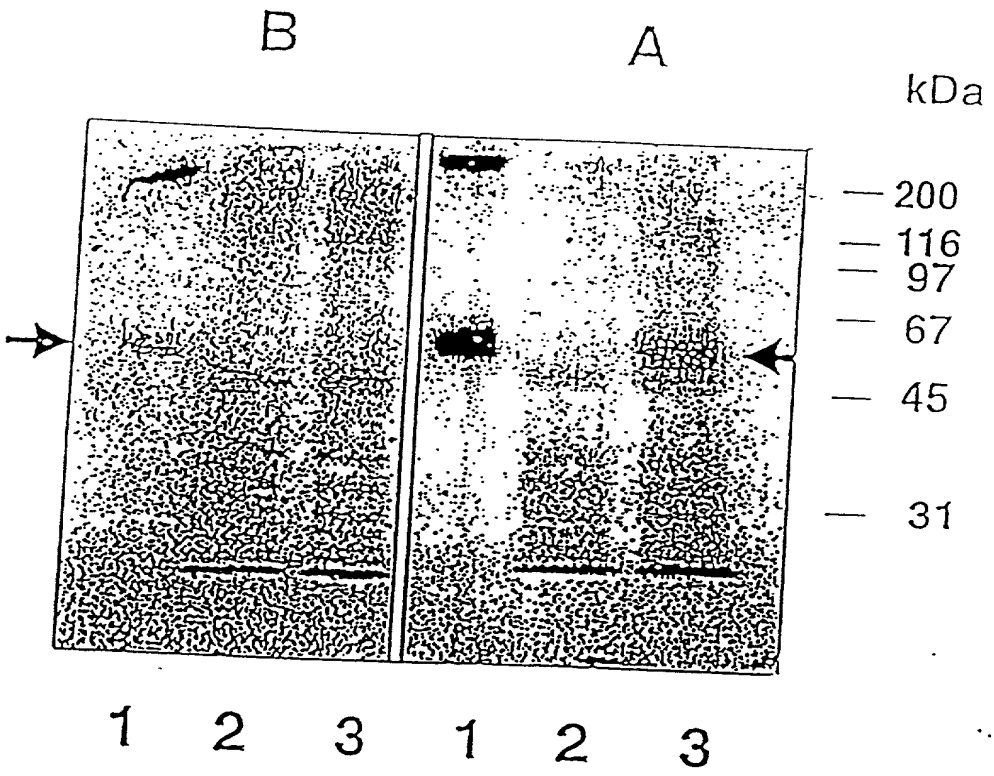


FIGURE 13

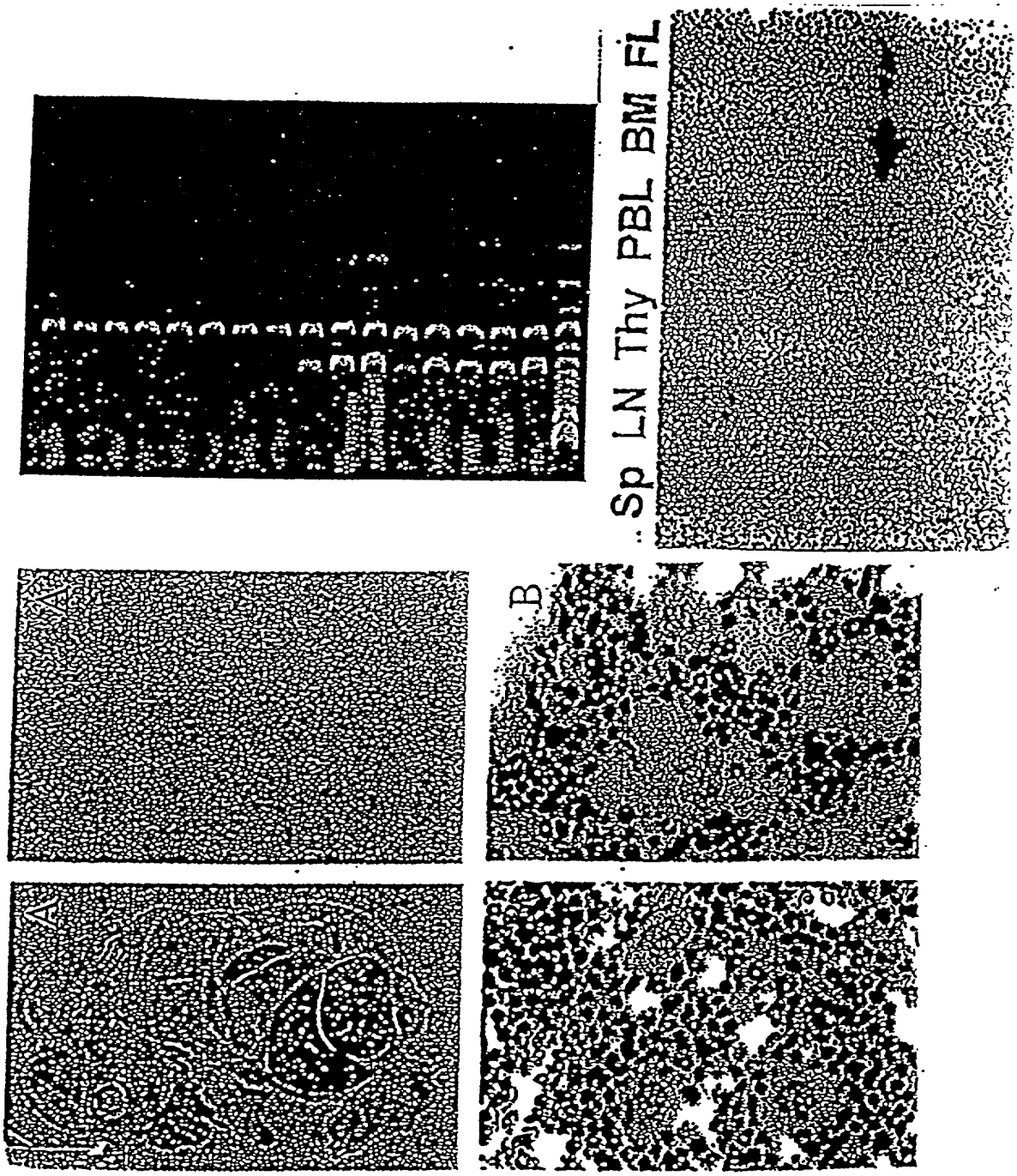


FIGURE 14

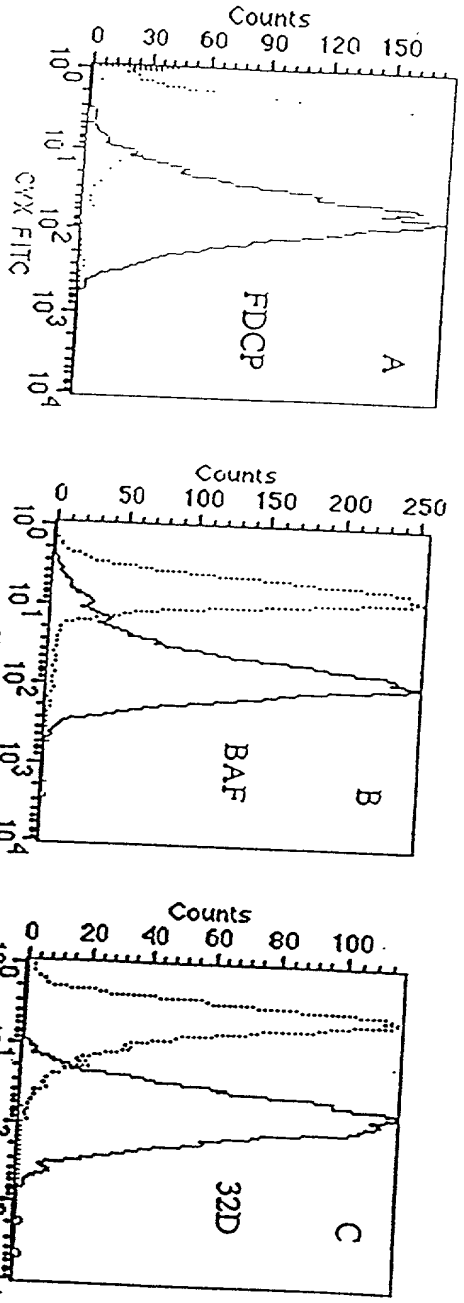

Counts
0 30 60 90 120 150
CYX FITC
FDCP
A
Counts
0 50 100 150 200 250
CYX FITC
BAF
B
Counts
0 20 40 60 80 100
CYX FITC
32D
C

FIGURE 15

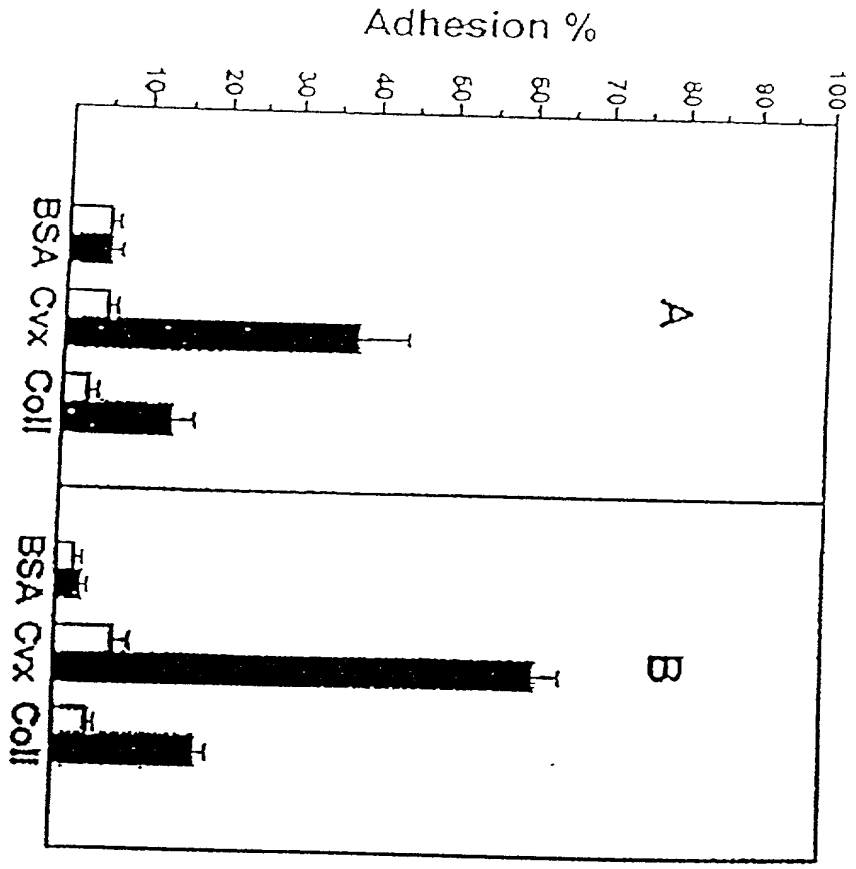

Adhesion %
10
20
30
40
50
60
70
80
90
100
BSA
Cvx
Coll
A
BSA
Cvx
Coll
B

FIGURE 16

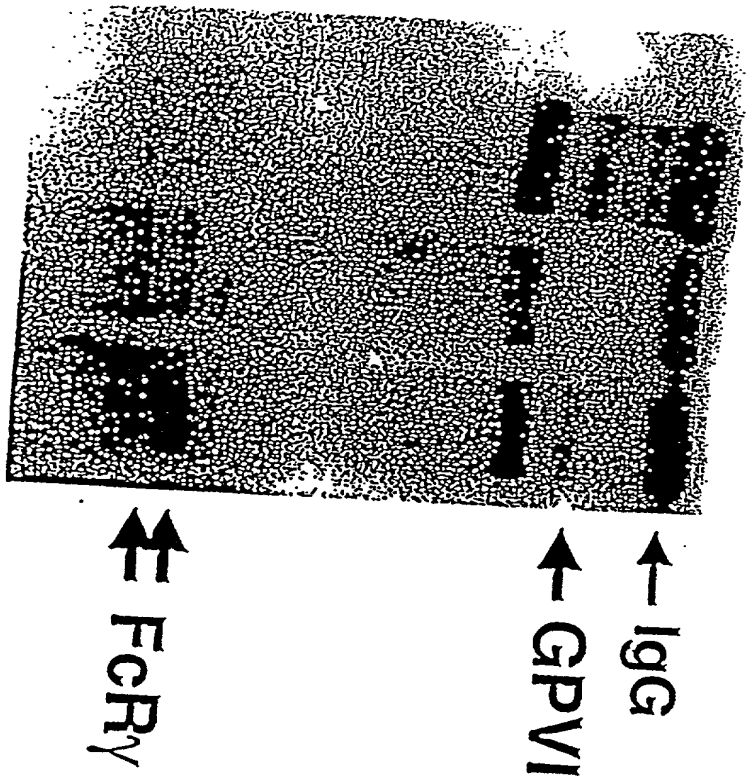


FIGURE 17

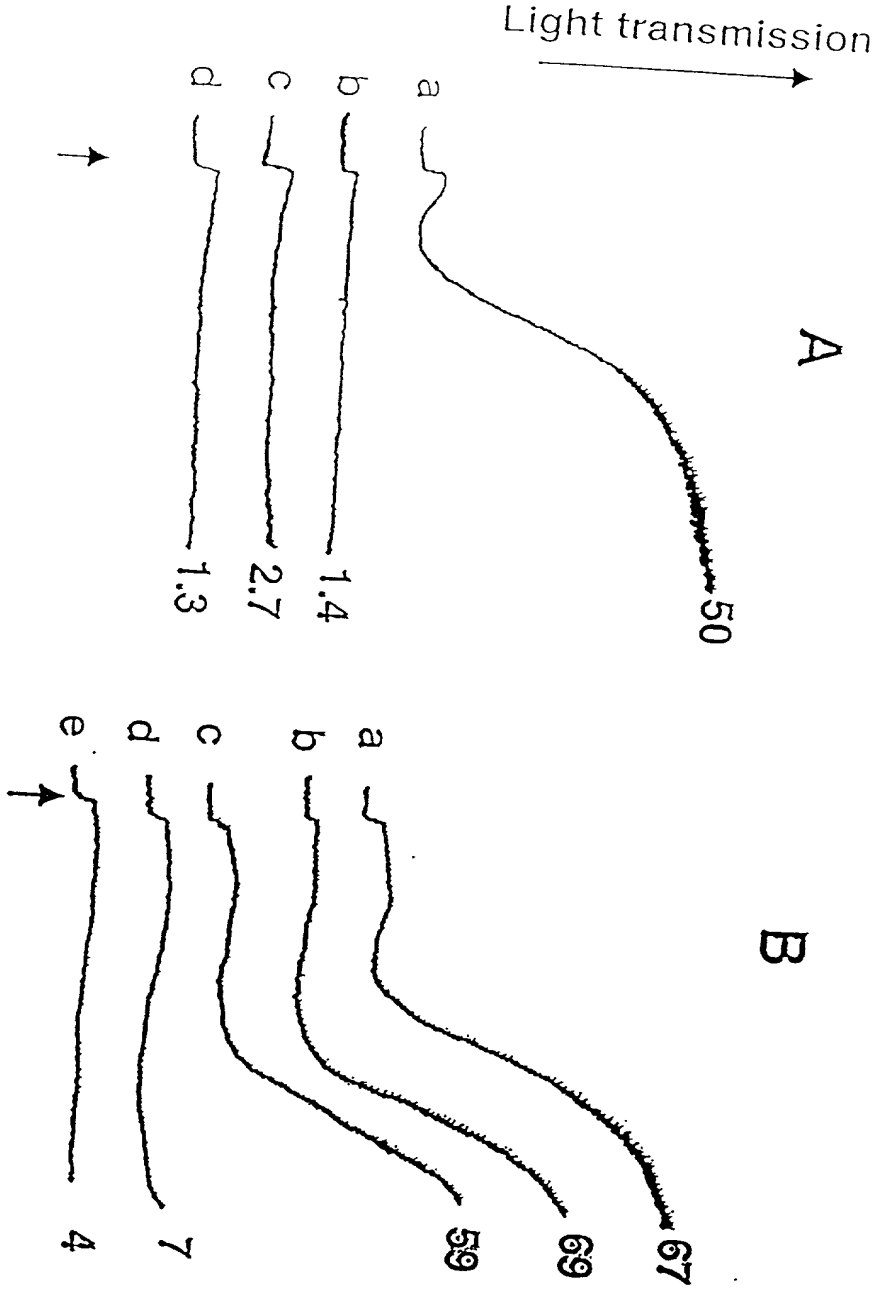


FIGURE 18

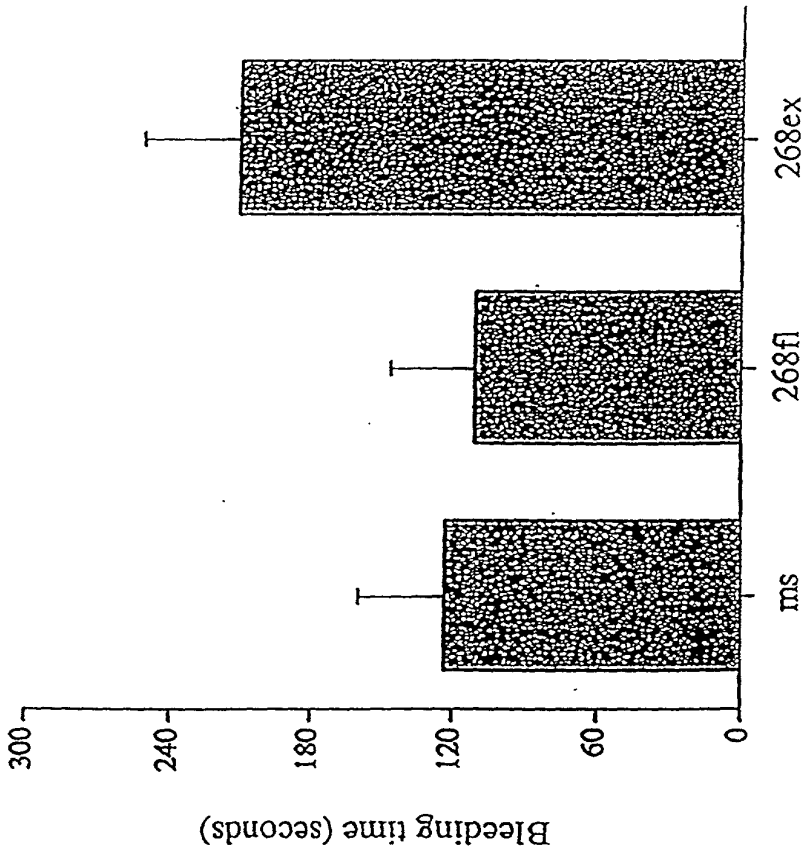

Bleeding time (seconds)
300
240
180
120
60
0
ms
268fl
268ex
Retroviruses

FIGURE 19

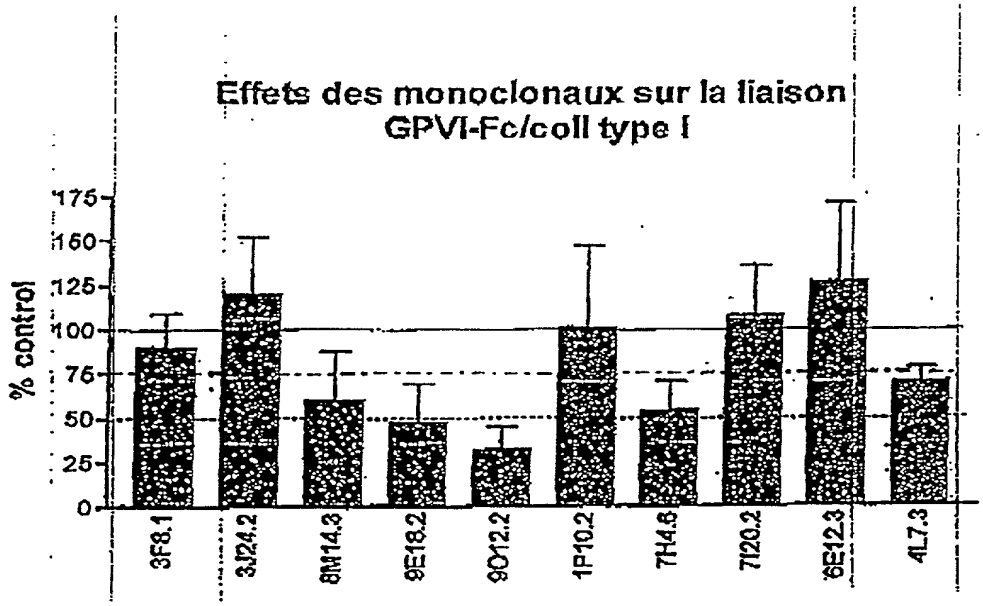

Effets des monoclonaux sur la liaison
GPVI-Fc/coll type I
% control
175
150
125
100
75
50
25
0
3F8.1
3J24.2
8M14.3
9E18.2
9O12.2
1P10.2
7H4.6
7I20.2
6E12.3
4L7.3

FIGURE 20

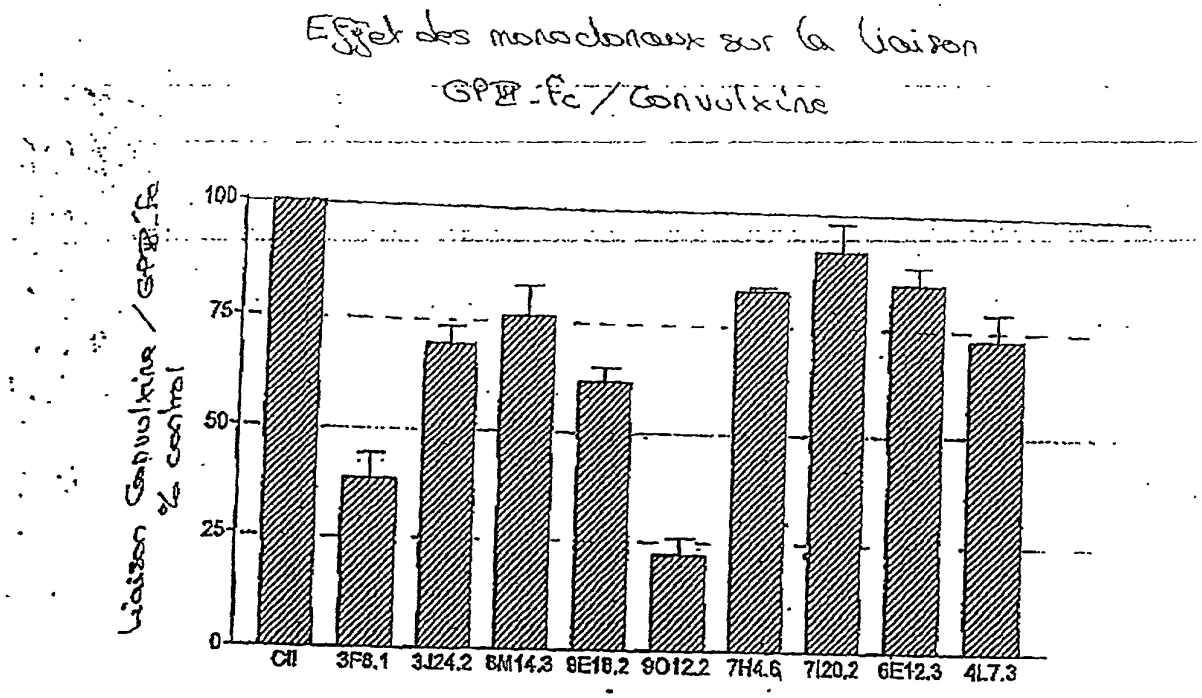
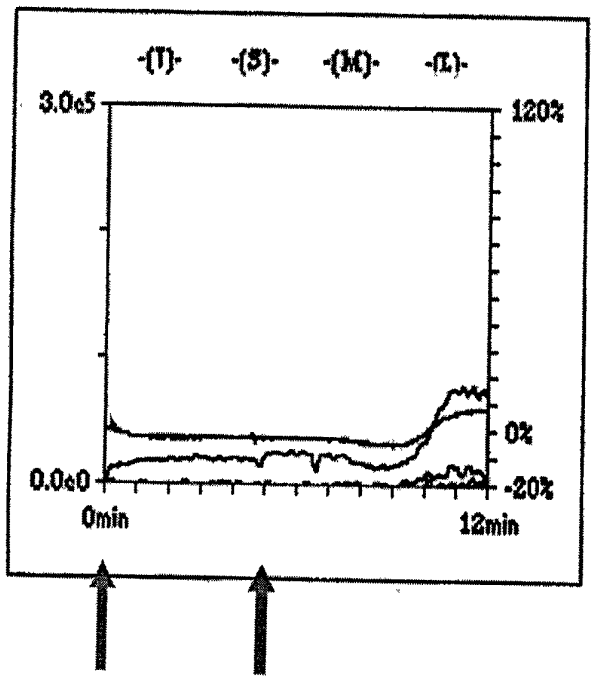
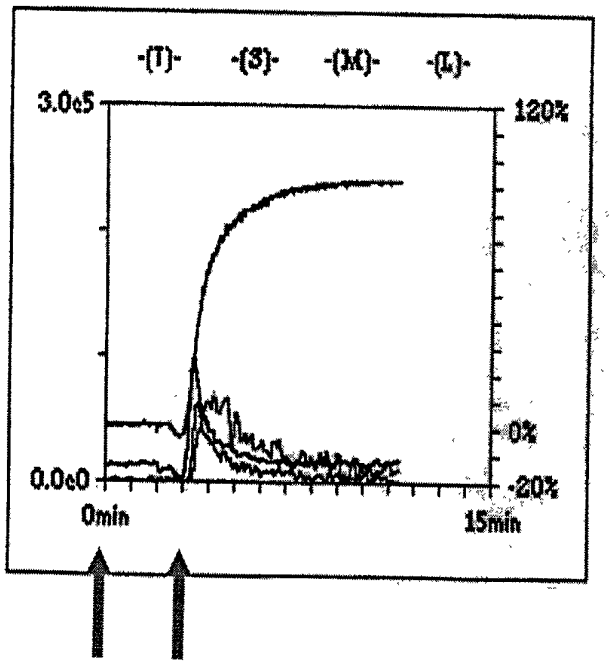

Effet des monoclonaux sur la liaison
GPIb-Fc / Convulxine
Liaison Convulxine / GPIb-Fc
% contrôl
100
75
50
25
0
Ctl
3F8.1
3J24.2
8M14.3
9E18.2
9O12.2
7H4.6
7I20.2
6E12.3
4L7.3

FIGURE 21

Template Selected



Fab collagen



PBScollagen

FIGURE 22

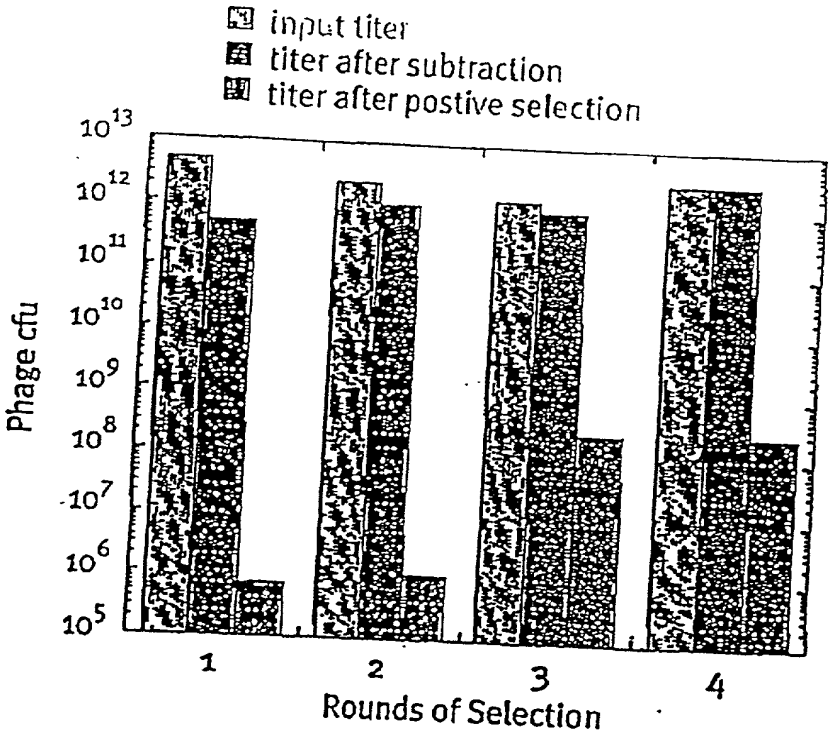

input titer
titer after subtraction
titer after postive selection
Phage cfu
10^{13}
10^{12}
10^{11}
10^{10}
10^{9}
10^{8}
10^{7}
10^{6}
10^{5}
1
2
3
4
Rounds of Selection

FIGURE 23

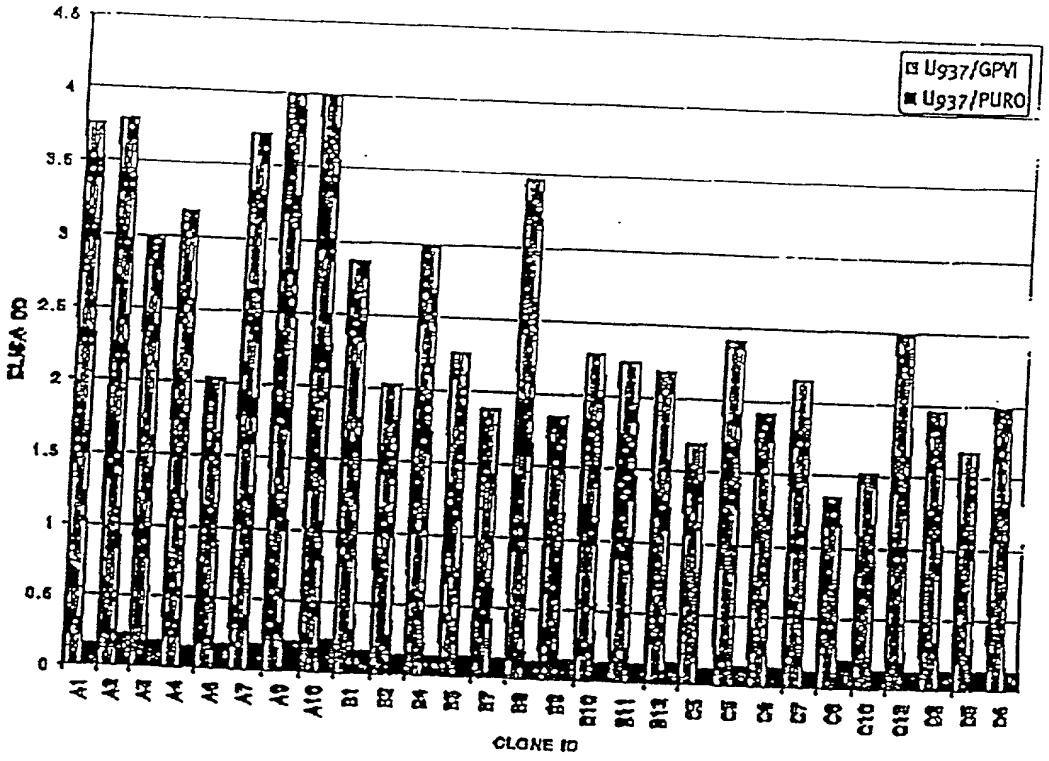

U937/GPVI
U937/PURO
ELISA OD
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
A1
A2
A3
A4
A6
A7
A9
A10
B1
B2
B4
B5
B7
B8
B9
B10
B11
B12
C3
C5
C6
C7
C8
C10
C12
D5
D7
D8
CLONE ID

FIGURE 24a

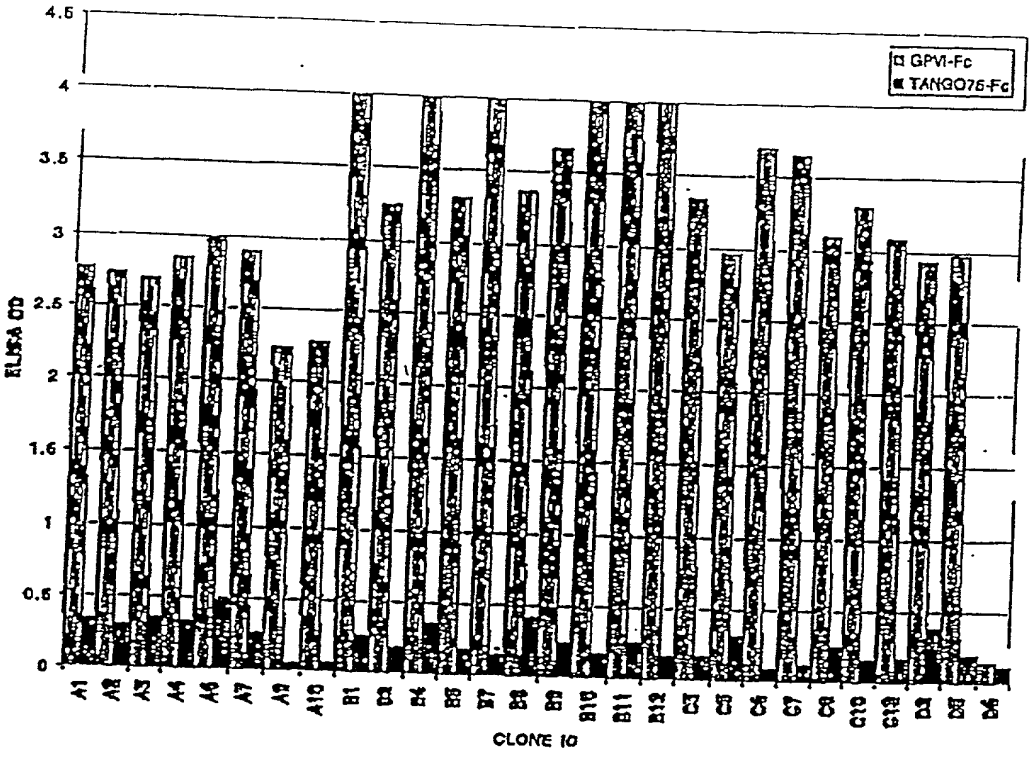


FIGURE 24b

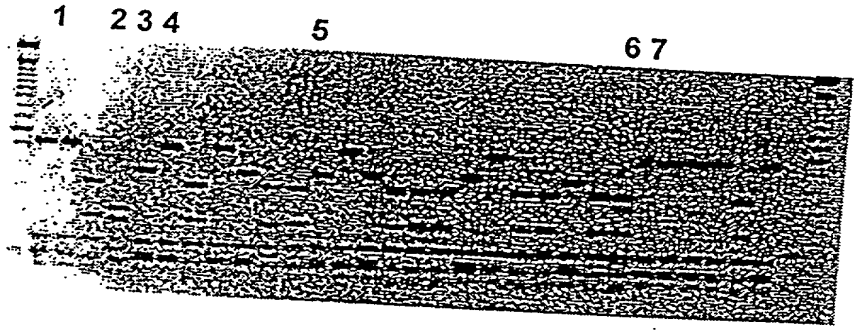
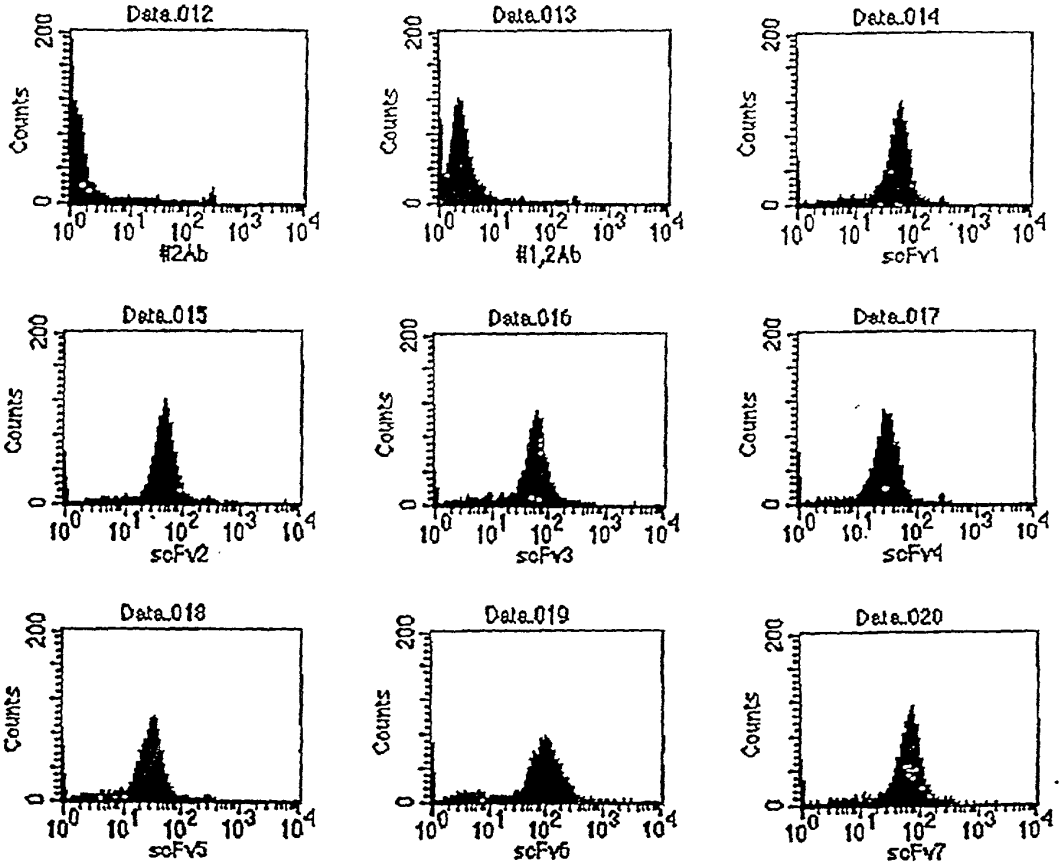


FIGURE 25



scFv1:A4
scFv2:B4
scFv3:A9
scFv4:C3
scFv5:C9
scFv6:C10
scFv7:A10

FIGURE 26

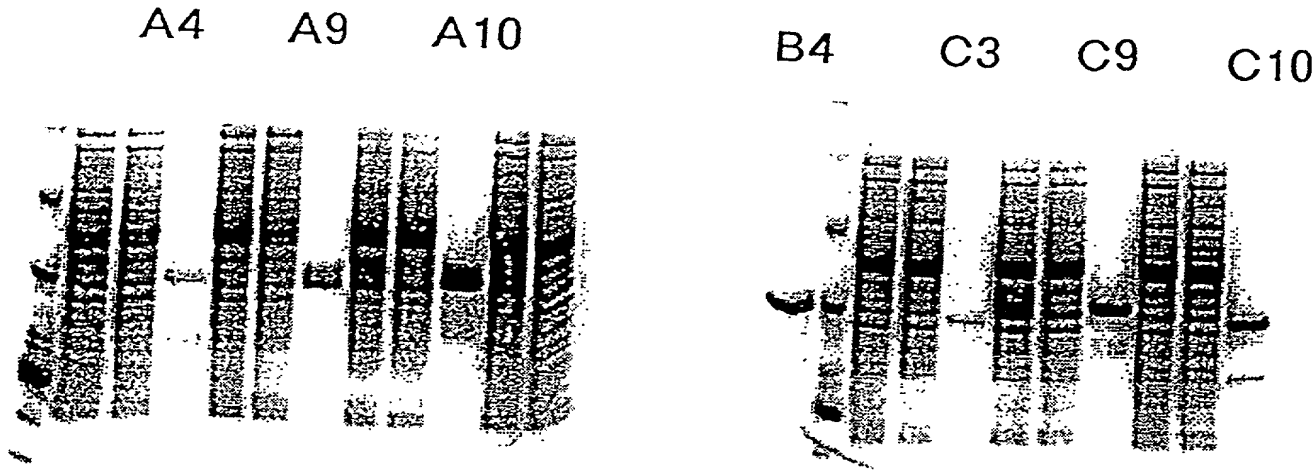


FIGURE 27

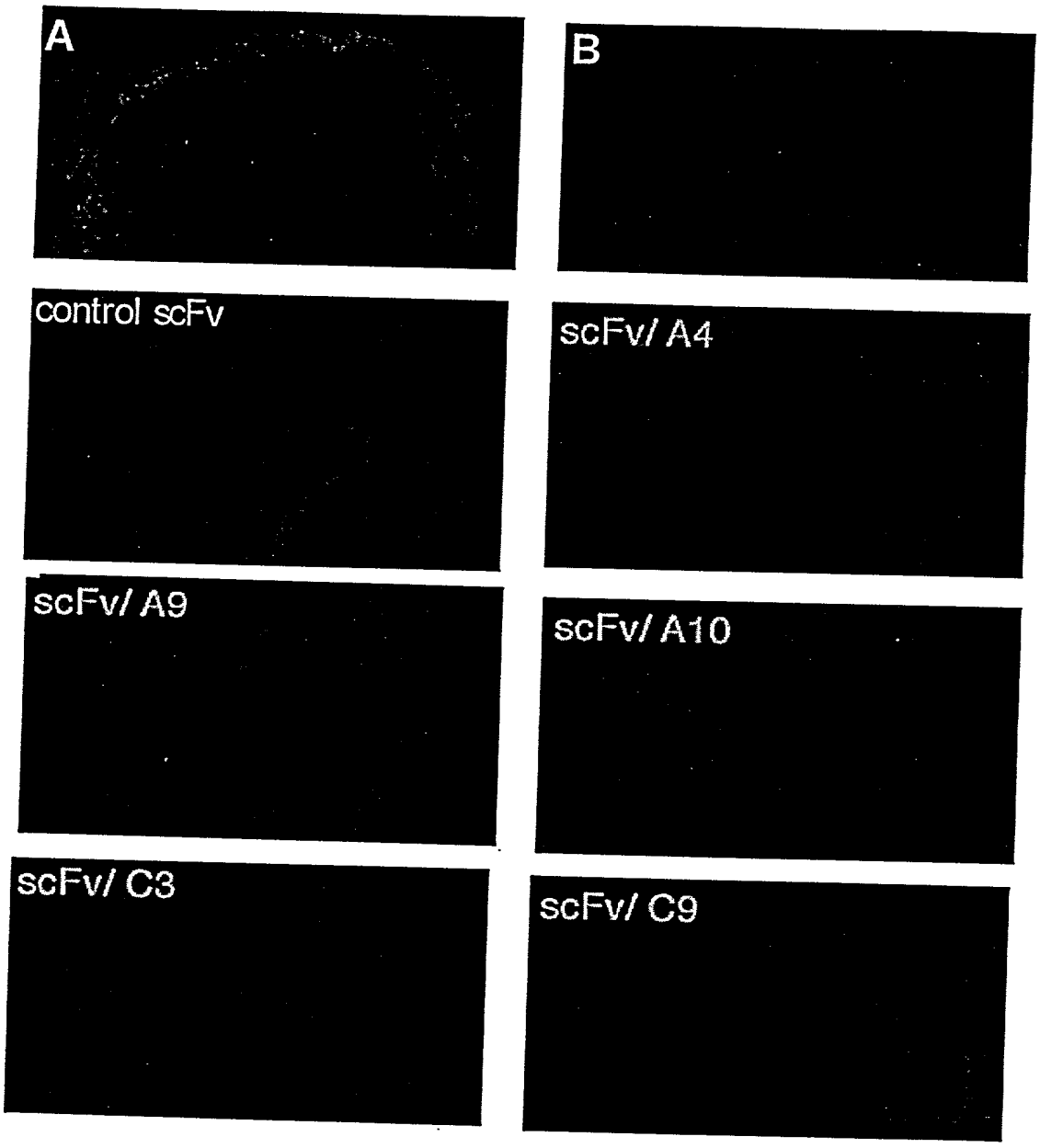


FIGURE 28

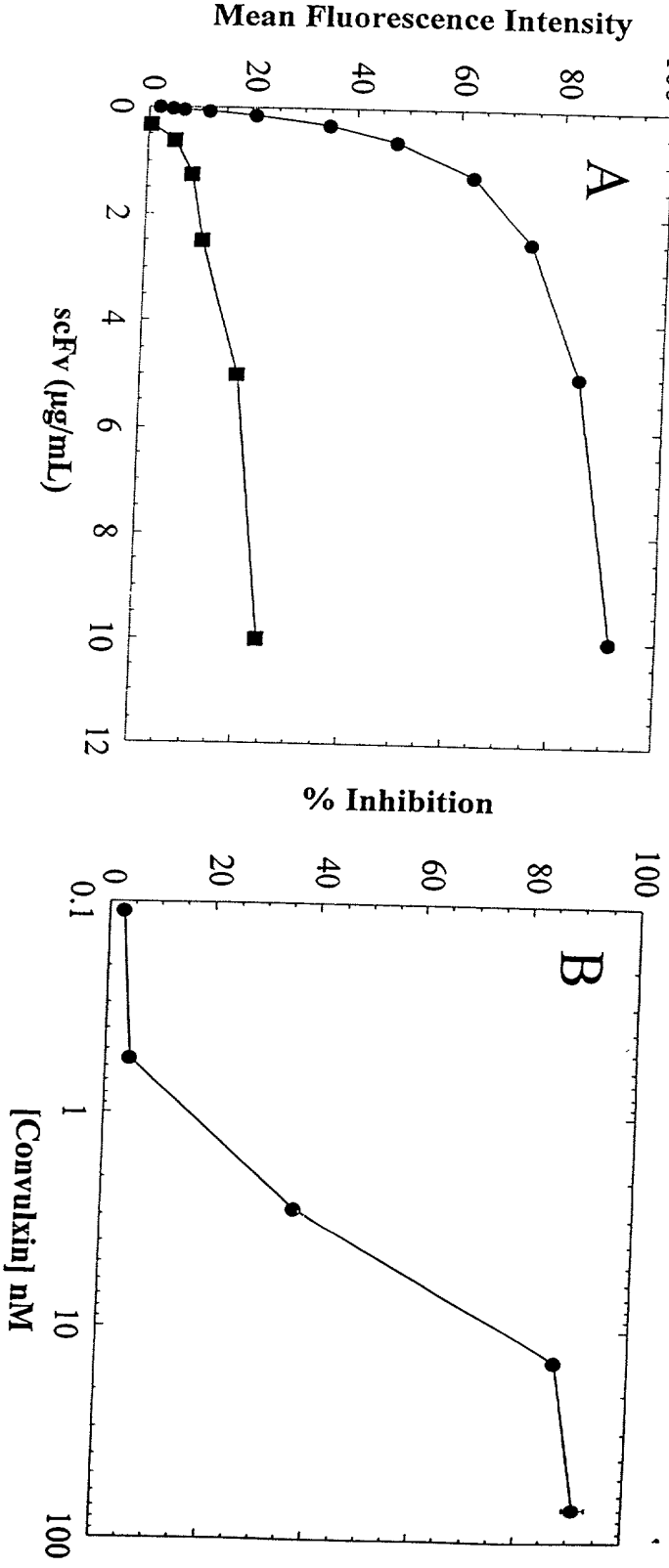

Mean Fluorescence Intensity
0
20
40
60
80
100
A
scFv (µg/mL)
0
2
4
6
8
10
12
% Inhibition
0
20
40
60
80
100
B
[Convulxin] nM
0.1
1
10
100

FIGURE 29

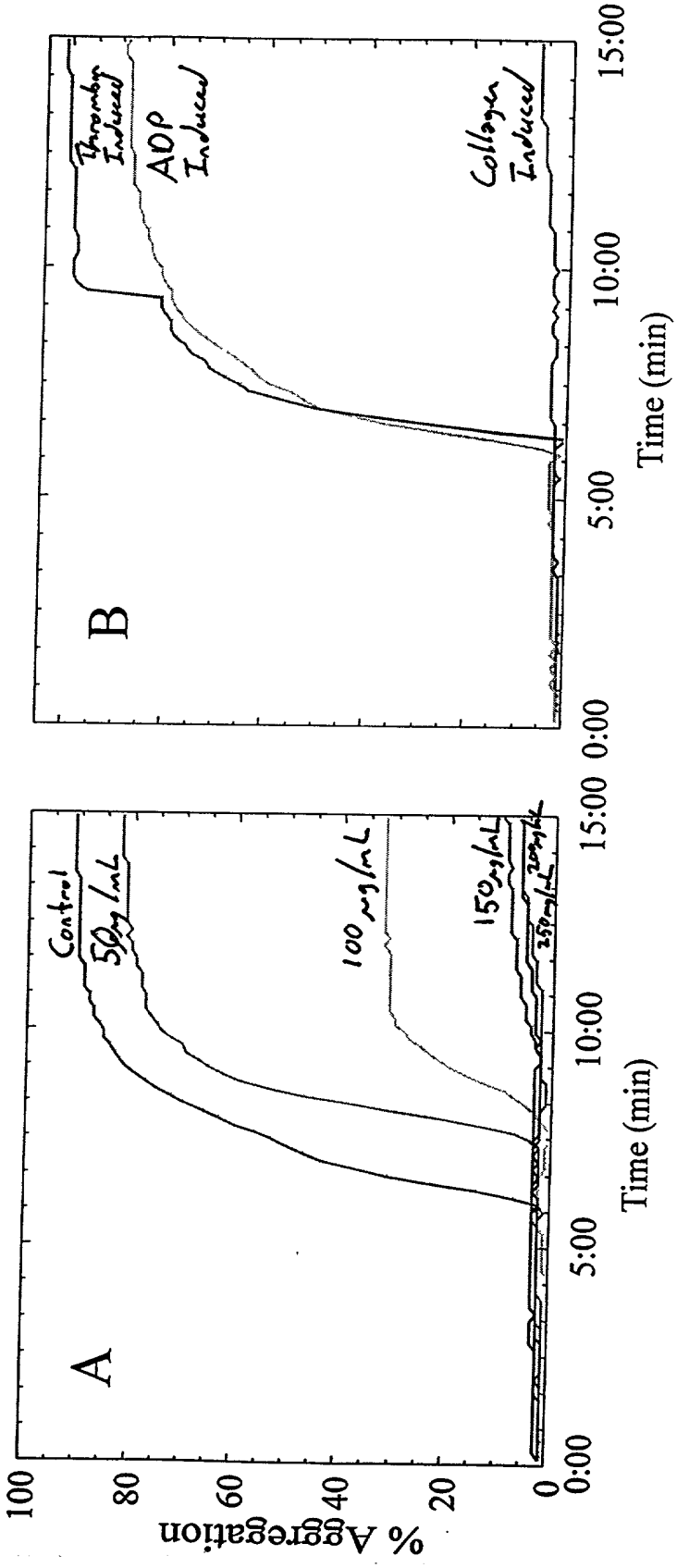

A
Control
50 mg/mL
100 mg/mL
150 mg/mL
250 mg/mL
% Aggregation
100
80
60
40
20
0
0:00
5:00
10:00
15:00
Time (min)
B
Thrombin Induced
ADP Induced
Collagen Induced
0:00
5:00
10:00
15:00
Time (min)

FIGURE 30